```
                  10        20        30        40        50        60        70
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
KP691596  GGA-GGCTTATTCTATATATATATATAG---TATAG--GCTT-TTCC-CACATACACAGCAAACTTTTAT
MK463629  GGA-GGCTTATTCTATATATATATATAG---TATAG--GCTT-TTCC-CACATACACAGCAAACTTTTAT
MK463628  GGAAGGCTTATTCTATATATATATATAG---TATAGC-GCTT-TTCC-CACATACACAGCACACTTTTGT
MK463621  GGAAGGCTTATTCTATATATATATATAG---TATAGC-GCTT-TTCC-CACATACACAGCACACTTTTAT
MK463622  GGGAGGCTTATTCTATATATATATATAG---TATAGC-GCTT-TTCC-CACATACACAGCACACTTTTAT
MK463627  AGGAGGCTTATTCTATATATATATATAG---TATAGC-GCTT-TTCC-CACATACACAGCACACTTTTAT
MK463625  AGGAGGCTTATTCTATATATATATATAG---TATAGC-GCTT-TTCC-CACATACACAGCACACTTTTAT
MK463623  GGGAGGCTTATTCTATATATATATATAG---TATGG--GCTT-TTCC-CACATACACAGCACACTTTTAT
MK463626  GAGAGCCTAAACTTCTATATATATATATCCGTATAGC-GCTTATTCC-CACATACACAGCACACTTTTAT
MK463624  GGGAGAGCTATTTTCTATATATATATAGCCTT-TCCC-GCTT-TTCC-CACATACACATCAAATTTTTAT
MK474651  GGGAGGCCTA---TATATAT-TATACATT-ATATAG--GCCTTTCCCACACATACACAGCAAACTTTTGT
MK474649  GGGAGGCCTA---TATATAT-TATACATT-ATATAGA-GCCTTTCCCACACATACACAGCAAACTTTTGT
MK474648  GGAAGGCCTA---TATATATATATACATT-ATATAGG-GCCTTTCCCACACATACACAGCAAACTTTTGT
MK474646  AGAAGGCCTA---TATATAT-TATACAGT-ATATAC--GCCTTCCCCACACATACACAGCAAACTTTTGT
MK474647  GGGAGGCCTA---TATATAT-TATACATT-ATATAG--GCCTTTCCCACACATACACAGCAAACTTTTGT
KY963132  GGGAGGCCTA---TATATAT-TATACATT-ATATAG--GCCTTTCCCACACATACACAGCAAACTTTTGT
MK474650  GGGAAGCCTA---TATATAT-TATACATT-ATATAG--GCCTTTCCCACACATACACAGCAAACTTTTGT
MK474652  AGGATGCCTA---TATATAT-TATACGTT-TTACCG--GCTTTTCCCCCCCTTACCCGTCAACCTTTTTT
MK474653  AGGAAGCCTA---TATATAT-TATACATT-TTATATAGGCCTTTCCCACACATACACAGCAAACTTTTGT
MK474642  GGGGAGACTA---TGTATATATATGTAG----------GCCTTTCCC--ACATACACAGCAAAGTTTTGT
MK474641  AAGGAGACTA---TGTATATATATGTAG----------GCCTTTCCC--ACATACACAGCAAAGTTTTGT
MG980399  GGGAGACCTA---TGTATATATATGTAG----------GCCTTTCCC--ACATACACAGCAAAGTTTTGT
MK474640  AGAAGACCTAA--TGTATATATATGTAG----------GCCTTTCCC--ACATACACAGCAAAGTTTTGT
JX898938  TAGAGAGTAGTAGAATACATCTACTCGGGGAGGCAT--GTTTTTTCC-----GATATGCCTTTCCCACAT

                  80        90       100       110       120       130       140
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
KP691596  ACTCGAAATTTGCAGTAAA-----AAAGGCCGATCGACGTTGTAGAACGCACCGCCTATAC--ACAAAAG
MK463629  ACTCGAAATTTGCAGTAAA-----AAAGGCCGATCGACGTTGTAGAACGCACCGCCTATAC--ACAAAAG
MK463628  ACTCGAAATTTGCAGTAAA-----AAAGGCCGATCGACGTTGTAGAACGCACCGCCTATAC--ACAAAAG
MK463621  ACTCGAAATTTGCAGTAAA-----AAGGGCCGATCGACGTTGTAGAACGCACCGCCTATAC--ACAAAAG
MK463622  ACTCGAAATTTGCAGTAAA-----AAAGGCCGATCGACGTTGTAGAACGCACCGCCTATAC--ACAAAAG
MK463627  ACTCGAAATTTGCAGTAAA-----AAGGGCCGATCGACGTTGTAGAACGCACCGCCTATAC--ACAAAAG
MK463625  ACTCGAAATTTGCAGTAAA-----AARGGCCGATCGACGTTGTAGAACGCACCGCCTATAC--ACAAAAG
MK463623  ACTCGATATTTGCAGTAAA-----AAGGGCCGATCGACGTTGTAGAACGCACCGCCTATAC--ACAAAAG
MK463626  ACTCGATATTTGCAGTAAA-----AAGCGCCGATCGACGTTGTAGAACGCACCGCCTATAC--ACAAAAG
MK463624  TCTCAATATTTGCAGGAAA-----AAG-GCCGATCGACGTTGTAGAACGCACCGCCCATAC--ACAAAAG
MK474651  ACTCGAAGTTTGCAGTAAACA---AAAGGCCGATCGACGTTATA--ACGCACCGCCTATAC--ACAAAAG
MK474649  ACTCGAAGTTTGCAGTAAACA---AAAGGCCGATCGACGTTATA--ACGCACCGCCTATAC--ACAAAAG
MK474648  ACTCGAAGTTTGCAGTAAACA---AAAGGCCGATCGACGTTATA--ACGCACCGCCTATAC--ACAAAAG
MK474646  ACTCTAAGTTTGCAGTAAACA---AAAGGCCTATCGACGTTATA--ACGCACCGCCTATAC--ACAAAAT
MK474647  ACTCGAAGTTTGCAGTAAACA---AAAGGCCGATCGACGTTATA--ACGCACCGCCTATAC--ACAAAAG
KY963132  ACTCGAAGTTTGCAGTAAACA---AAAGGCCGATCGACGTTATA--ACGCACCGCCTATAC--ACAAAAG
MK474650  ACTCGAAGTTTGCAGTAAACA---AAAGGCCGATCGACGTTATA--ACGCACCGCCTATAC--ACAAAAG
MK474652  ACTCAAAATTTGCGCTAAACA---AAAGGCCAACCCACCTTATA--ACCCACCGCCTTTCC--ACAAAAT
MK474653  ACTCGAAGTTTGCAGTAAACA---AAAGGCCAATCAACGTTATA--ACCCACCCCCAATAC--ACAAAAC
MK474642  ACTCAAAATTTGCAGTAAAAA---AAAGGCCGATCGACGTTATA--ACGCACCGCCTAT----ACAAAAG
MK474641  ACTCAAAATTTGCAGTAAAAA---AAAGGCCGATCGACGTTATA--ACGCACCGCCTAT----ACAAAAG
MG980399  ACTCAAAATTTGCAGTAAAAA---AAAGGCCGATCGACGTTATA--ACGCACCGCCTAT----ACAAAAG
MK474640  ACTCAAAATTTGCAGTAAAAA---AAAGGCCGATCGACGTTATA--ACGCACCGCCTAT----ACAAAAG
JX898938  ACACAAACACAGCAATATATATGTATATATATACGTATATTGCTATACCCAAAAACCATACCGTAAAAAG

                 150       160       170       180       190       200       210
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|
KP691596  CAAAAATGTCCGTTTATACAAAA------AAATAGACGGCGTTTCGGTT--TTTGGCGGGAGGGAGAGAG
MK463629  CAAAAATGTCCGTTTATACAAAA------AAATAGACGGCGTTTCGGTT--TTTGGCGGGAGGGAGAGAG
MK463628  CAAAAATGTCCGTTTATACAAAA------AAATAGACGGCGTTTCGGTT--TTTGGCGGGAGGGAGAGAG
MK463621  CAAAAATGTCCGTTTATACAAAA------AAATAGACGGCGTTTCGGTT--TTTGGCGGGAGGGAGAGAG
MK463622  CAAAAATGTCCGTTTATACAAAA------AAATAGACGGCGTTTCGGTT--TTTGGCGGGAGGGAGAGAG
MK463627  CAAAAATGTCCGTTTATACAAAA------AAATAGACGGCGTTTCGGTT--TTTGGCGGGAGGGAGAGAG
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MK463625  CAAAAATGTCCGTTTATACAAAA------AAATAGACGGCGTTTCGGTT--TTTGGCGGGAGGGAGAGAG
MK463623  CAAAAATGTCCGTTTATACAAAA------AAATAGACGGCGTTTCGGTT--TTTGGCGGGGGGGAGAGAG
MK463626  CAAAAATGTCCGTTTATACAAAA------ATATAGACTGCGTTTCGGTT--TTTGGCGGGAGGGAGAGAG
MK463624  CAAAATTGTCCGTTTATACAAAA------ATATAGACTGTGTTTCGGTT--TTTGGCGGGGGGGAGAGAG
MK474651  CAAAAATGTCCGTTTATACAAA----------TATACGGCGTTTCGGTT--TT------------GTTGG
MK474649  CAAAAATGTCCGTTTATACAAA----------TATACAGCGTTTCGGTT--TT------------GTTGG
MK474648  CAAAAATGTCCGTTTATACAAA----------TATACTGCTTTTCGGTT--TT------------GTTGG
MK474646  CTAAAATGTCCGTTTATACAAA----------TATACTGCTTTTCGGTT--TT------------GGTGG
MK474647  CAAAAATGTCCGTTTATACAAA----------TATACGGCGTTTCGGTT--TT------------GTTGG
KY963132  CAAAAATGTCCGTTTATACAAA----------TATACGGCGTTTCGGTT--TT------------GTTGG
MK474650  CAAACATGTCCGTTTATACAAA----------TATACGGCGTTTCGGTT--TT------------GTTGG
MK474652  CAAACATGTCCTTTTATACAAT----------TATACGGCTTTCCGGTT--TT------------GTTGG
MK474653  CAAACATGTCCGTTTATACAAA----------TATACGGCGTTTCGGTT--TT------------GTTGG
MK474642  CAAAAATGTCCGTTTATACAAAA------A-ATATACGGCGTTTCGGTT--TT--------------TGG
MK474641  CAAAAATGTCCGTTTATACAAAA------A-ATATACGGCGTTTCGGTT--TT--------------TGG
MG980399  CAAAAATGTCCGTTTATACAAAA------A-ATATACGGCGTTTCGGTT--TT--------------TGG
MK474640  CAAAAATGTCCGTTTATACAAAA------A-ATATACGGCGTTTCAGTT--TT--------------TGG
JX898938  CAAAAAGGCCGGTCGACGCCAAATGCCGCGCGTATACAGTGGAAAAGTCCGTTCGTTACGGCTCTTTCTC

                  220       230       240       250
          ....|....|....|....|....|....|....|....|....|...
KP691596  AGGGGGGTGCGTGCGCGT-GGATAACGGCTCA-CATAA-CGTGTCGCG
MK463629  AGGGGGGTGCGTGCGCGT-GGATAACGGCTCA-CAT------------
MK463628  AGGGGGGTGCGTGCGCGT-GGATAACGGCTCA-CATAAACGTGTCAGC
MK463621  AGGGGGGTGCGTGCGCGT-GGATAACGGCTCA--ATAAACGTGTCACA
MK463622  AGGGGGGTGCGTGCGCGT-GGATAACGGCTCA-ATAAACCGTGTCACA
MK463627  AGGGGGGTGCGTGCGCGT-GGATAACGGCTCA-CATAAACGTGTCACA
MK463625  AGGGGGGTGCGTGCGCGT-GGATAACGGCTCA--CATAACGTGTCACA
MK463623  AGGGGGGTGCGTGCGCGT-GGATAACGGCTCA--ATAA-CGTGTCACA
MK463626  AGGGGGGGGCGTGCGCGTAGGATAACGGCTCACATAAACGGTGTCACA
MK463624  AGGGGGGG-CGTGC-------ATAACGGCTCA----AAGCATGTCACA
MK474651  CGGGGGGTGCGTGTGTGT-GGATAACGGCTCA-CATAAACGTGTCGCA
MK474649  CGGGGGGTGCGTGTGTGT-GGATAACGGCTCA--ATAAACGTGTCACA
MK474648  CGGGGGGTGCATGTGTGT-GGATAACGGCTCA-CATAAACGTGTCGCA
MK474646  CGGGGGGTGCATGTGTGT-GGACGCA----------------------
MK474647  CGGGGGGTGCGTGTGTGT-GGATAACGGCTCA-CATAA-CGTGTCGCA
KY963132  CGGGGGGTGCGTGTGTGT-GGATAACGGCTCA-CATAA-CGTGTCGCG
MK474650  TGGGGGGTGCGTATGTGT-GGATAACGGCTCA-CATAA-CGTGTCGCA
MK474652  TGGGGGGAGCATGGGTGT-GAATAACGGCTCC-AATAA-CGTGCCCAA
MK474653  GGGGGGGTGCGTGTGTGT-GGATAACGGCTCA-TTAAAC---------
MK474642  CGGGGTGGGTGCGTGTGT-GGATAACGGCTCA-CATAA-CGTGTCGCA
MK474641  CGGGGTGGGTGCGTGTGT-GGATAACGGCTCA-CATAA-CGTGTCGCA
MG980399  CGGGGTGGGTGCGTGTGT-GGATAACGGCTCA-CATAA-CGTGTCGCA
MK474640  CGGGGTGGGTGCGTGTGT-GGATAACGGCTCACATAAAACGTGTCGCA
JX898938  TCTCGCGGGTGTGTGTGT-GGATAACGGCTCA-CATAA-CGTGTCGCG
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